In response to the Office Action dated August 18, 2003 (Paper No. 14), please amend the application as follows.

a.) Amendments to the Claims

1. (Currently Amended) A polypeptide having an activity to transfer fucose to an N-acetylglucosamine residue in an N-acetyllactosamine (Galβ1-4GlcNAc) structure existing in a nonreducing terminus of a sugar chain via an α1,3-linkage, but not having an activity to transfer fucose to an N-acetylglucosamine residue in an α 2,3-sialyl N–acetyllactosamine (NeuAc α 2-3Gal β 1-4GlcNAc) structure existing in a nonreducing terminus of a sugar chain via an α 1,3-linkage, and which is ~~derived~~ obtained from mouse or human cells.

2. (Previously Presented) A polypeptide selected from the following (a) and b):

(a) a polypeptide comprising the amino acid sequence represented by SEQ ID NO:1 or 2,

(b) a polypeptide comprising the amino acid sequence of residues 56 to 359 represented by SEQ ID NO:1 or 2.

3. (Previously Presented) The polypeptide according to claim 1, wherein the activity of transferring fucose to an N-acetylglucosamine residue in the Gal β 1-4GlcNAc structure existing in a nonreducing terminus of a sugar chain via an α 1,3-linkage is the Lewis x sugar chain [Gal β 1-4(Fuc α 1-3)GlcNAc] and the Lewis y sugar chain [Fuc α 1-2Gal β 1-4(Fuc α 1-3)GlcNAc] synthesizing activity, and the activity of transferring fucose to an N-acetylglucosamine residue in the NeuAc α 2-3Gal β 1-4GlcNAc structure existing in a nonreducing terminus of a sugar chain via an α 1,3-linkage is the sialyl Lewis x sugar chain [NeuAc α 2-3Gal β 1-4(Fuc α 1-3)GlcNAc] synthesizing activity.

4. (Previously Presented) A DNA selected from the following (a), (b), (c), (d), (e), (f), (g) and (h):

(a) a DNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51,

(b) a DNA having nucleotides 280 to 1194 of a nucleotide sequence represented by SEQ ID NO: 3,

(c) a DNA having nucleotides 115 to 1194 of a nucleotide sequence represented by SEQ ID NO: 3,

(d) a DNA having nucleotides 1454 to 2368 of a nucleotide sequence represented by SEQ ID NO: 4,

(e) a DNA having nucleotides 1289 to 2368 of a nucleotide sequence represented by SEQ ID NO: 4,

(f) a DNA having nucleotides 460 to 1374 of a nucleotide sequence represented by SEQ ID NO: 5,

(g) a DNA having nucleotides 295 to 1374 of a nucleotide sequence represented by SEQ ID NO: 5,

(h) a DNA hybridizing with DNA selected from (a), (b), (c), (d), (e), (f) and (g) using a filter with colony- or plaque-derived DNA immobilized thereon at 65°C in the presence of 0.7-1.0M of NaCl, followed by washing the filter at 65°C with 0.1-2.0 standard concentration of SSC (saline-sodium citrate) solution (one standard concentration of SSC solution consists of 150mM sodium chloride and 15mM sodium citrate), said DNA encoding a polypeptide having an activity to transfer fucose to an N-acetylglucosamine residue in an N-acetyllactosamine (Gal β 1-4GlcNAc) structure existing in a nonreducing terminus of a sugar chain via an α 1,3-linkage, but not having an activity to transfer fucose to an α 2,3-sialyl N-acetyllactosamine (NeuAc α 2-3Gal β 1-4GlcNAc) structure existing in a nonreducing terminus of a sugar chain via an α 1,3-linkage.

5. (Original) A recombinant DNA obtained by integrating the DNA according to claim 4 into a vector.

6. (Previously Presented) The recombinant DNA according to claim 5 wherein the recombinant DNA is plasmid pAMo-mFT9 or plasmid pBS-hFT9 (S2).

7. (Previously Presented) A non-human transformant or a transformant cell having the recombinant DNA according to claim 5.

8. (Previously Presented) The transformant according to claim 7 or 52, wherein the transformant is selected from the group consisting of microorganisms, animal cells, plant cells, insect cells, non-human transgenic animals, and transgenic plants.

9. (Previously Presented) The transformant according to claim 8, wherein the microorganism belongs to *Escherichia*.

10. (Previously Amended) The transformant according to claim 8, wherein the animal cell is selected from the group consisting of mouse myeloma cells, rat myeloma cells, mouse hybridoma cells, CHO cell, BHK cell, African green monkey kidney cells, Namalwa cell, Namalwa KJM-1 cell, human fetal kidney cells, and human leukemia cells.

11. (Previously Presented) The transformant according to claim 8, wherein the insect cell is selected from the group consisting of *Spodoptera frugiperda* ovarian cells, *Trichoplusia ni* ovarian cells, and silkworm ovarian cells.

12. (Previously Presented) A method for producing a polypeptide according to any one of claims 1, 2, 3 and 51, which comprises the steps of:

culturing in a medium a transformant having a recombinant DNA obtained by inserting a DNA encoding the polypeptide into a vector;

producing and accumulating said polypeptide in said medium; and

isolating said polypeptide from the medium.

13. (Previously Presented) A method for producing a polypeptide according to any one of claims 1, 2, 3 and 51, which comprises the steps of:

feeding a non-human transgenic animal having a recombinant DNA obtained by inserting a DNA encoding the polypeptide into a vector;

producing and accumulating said polypeptide in said medium; and

isolating said polypeptide from the animal.

14. (Original) The method for producing the polypeptide according to claim 13, wherein the production and accumulation of said polypeptide is carried out in the milk of said non-human transgenic animal.

15. (Previously Presented) A method for producing a polypeptide according to any one of claims 1, 2, 3 and 51, which comprises the steps of:

growing a transgenic plant having a recombinant DNA obtained by inserting a DNA encoding the polypeptide into a vector;

producing and accumulating said polypeptide in said medium; and

isolating said polypeptide from the plant.

16. (Previously Presented) A method for producing a polypeptide according to any one of claims 1, 2, 3 and 51, which comprises the steps of:

using a DNA encoding the polypeptide, and

synthesizing said polypeptide by an *in vitro* transcription-translation system.

17. (Previously Presented) A method for producing a reaction product wherein fucose is added to an N-acetylglucosamine residue in the N-acetyllactosamine structure of an acceptor substrate via an α 1,3-linkage, using a polypeptide selected from a polypeptide according to any one of claims 1, 2, 3 and 51 as an enzyme source, which comprises the steps of:

placing in an aqueous medium (a) said enzyme source, (b) an

acceptor substrate selected from (i) N-acetyllactosamine(Gal β 1-4GlcNAc), (ii) oligosaccharides having the N-acetyllactosamine structure in a nonreducing terminus thereof, (iii) complex carbohydrates having the N-acetyllactosamine structure in a nonreducing terminus of sugar chains, (iv) their derivatives wherein the N-acetyllactosamine structure is modified by sulfate group, and (v) their derivatives wherein the N-acetyllactosamine structure is modified by sugar, but a galactose residue in the N-acetyllactosamine structure is not modified by sialic acid via an α 2,3-linkage, and (c) guanosine-5'-diphosphate fucose;

producing and accumulating the reaction product, in the aqueous medium; and

collecting said reaction product from said aqueous medium.

18. (Previously Presented) The method for producing the reaction product according to claim 17, wherein a derivative is selected from sugar chains having, in a nonreducing terminus thereof, any one of the following oligosaccharide structures: Fuc α 1-2Gal β 1-4GlcNAc, Gal α 1-3Gal β 1-4GlcNAc, Gal α 1-3(Fuc α 1-2)Gal β 1-4GlcNAc, GalNAc α 1-3(Fuc α 1-2)Gal β 1-4GlcNAc, Gal α 1-4Gal β 1-4GlcNAc, Gal β 1-4GlcNAc(6S0$_3^-$); and complex carbohydrates containing said sugar chains.

19. (Previously Presented) A method for producing a reaction product wherein fucose is added to a glucose residue in a lactose structure of an acceptor substrate via an α 1,3-linkage, using a polypeptide according to any one of claims 1, 2, 3 and 51 as an enzyme source, which comprises the steps of:

placing in an aqueous medium (a) said enzyme source, (b) an acceptor substrate selected from (i) lactose (Gal β 1-4Glc), (ii) oligosaccharides having a lactose structure in a nonreducing terminus thereof, (iii) complex carbohydrates having a lactose structure in a nonreducing terminus of sugar chains, (iv) their derivatives wherein a lactose structure is modified by sulfate group, and (v) their derivatives wherein a lactose structure is modified by sugar(s), but a galactose residue in the lactose structure is not modified by

sialic acid via an α 2,3-linkage, and (c) guanosine-5' -diphosphate fucose;

producing and accumulating the reaction product, in said aqueous medium; and

collecting said reaction product from said aqueous medium.

20. (Previously Presented) The method for producing the reaction product according to claim 19, wherein a derivative is selected from sugar chains having, in a nonreducing terminus thereof, any one of the following oligosaccharide structures: Gal α 1-3Gal β 1-4Glc, Gal α 1-3(Fuc α 1-2)Gal β 1-4Glc, GalNAc α 1-3(Fuc α 1-2)Gal β 1-4Glc, Gal α 1-4Ga1 β 1-4Glc, Gal β 1-4Glc(6SO_3^-); and complex carbohydrates containing said sugar chains.

21. (Previously Presented) A method for producing a sugar chain having a structure wherein fucose is added to an N-acetylglucosamine residue or a glucose residue via an α 1,3-linkage, or a complex carbohydrate containing said sugar chain, which comprises the steps of:

culturing in a medium a transformant selected from the transformants derived from microorganisms, animal cells, plant cells, and insect cells according to claim 8;

producing and accumulating the sugar chain or the complex carbohydrate in said medium; and

collecting said sugar chain or said complex carbohydrate from said medium.

22. (Previously Presented) A method for producing a sugar chain having structure wherein fucose is added to an N-acetylglucosamine residue or a glucose residue via an α 1,3-linkage, or a complex carbohydrate containing said sugar chain, which comprises the steps of:

feeding a nonhuman transgenic animal according to claim 8;

producing and accumulating the sugar chain or the complex carbohydrate in

the non-human transgenic animal; and

collecting said sugar chain or said complex carbohydrate from said non-human transgenic animal.

23. (Previously Presented) A method for producing a sugar chain having a structure wherein fucose is added to an N-acetylglucosamine residue or a glucose residue via an α 1,3-linkage, or a complex carbohydrate containing said sugar chain, which comprises the steps of:

growing a transgenic plant according to claim 8;

producing and accumulating the sugar chain or the complex carbohydrate in said transgenic plant; and

collecting said sugar chain or said complex carbohydrate from said transgenic plant.

24. (Previously Presented) The production method according to claim 17, wherein the complex carbohydrate is selected from the group consisting of glycoproteins, glycolipids, proteoglycans, glycopeptides, lipopolysaccharides, peptideglycans and glycosides wherein a sugar chain binds to compounds such as steroids.

25. (Previously Presented) The method for producing the sugar chain or the complex carbohydrate according to claim 22, wherein the generation and accumulation of said sugar chain or said complex carbohydrate is carried out in the milk of said non-human transgenic animal.

26. (Previously Presented) A method for determining the expression level of a gene encoding a polypeptide according to any one of claims 1, 2, 3 and 51, by hybridization using DNA encoding the polypeptide.

27. (Previously Presented) An oligonucleotide selected from the following

oligonucleotides: an oligonucleotide having an identical sequence to 10 to 50 contiguous nucleotides in a nucleotide sequence of DNA selected from a DNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51; a DNA having the nucleotide sequence represented by SEQ ID NO: 3; a DNA having the nucleotide sequence represented by SEQ ID NO: 4; and a DNA having the nucleotide sequence represented by SEQ ID NO: 5; and, an oligonucleotide having a complementary sequence to said oligonucleotide and a derivative of each of said oligonucleotides.

28. (Original) The oligonucleotide according to claim 27, wherein said oligonucleotide derivative is selected from the following oligonucleotide derivatives: an oligonucleotide derivative obtained by converting a phosphodiester bond into a phosphorothioate bond in an oligonucleotide; an oligonucleotide derivative obtained by converting a phosphodiester bond into a N3'-P5' phosphoamidate bond in an oligonucleotide; an oligonucleotide derivative obtained by converting a ribose and phosphodiester bond into a peptide-nucleic-acid bond in an oligonucleotide; an oligonucleotide derivative obtained by substituting uracil with C-5 propynyl uracil in an oligonucleotide; an oligonucleotide derivative obtained by substituting uracil with C-5 thiazolyl uracil in an oligonucleotide; an oligonucleotide derivative obtained by substituting cytosine with the C-5 propynylcytosine in an oligonucleotide; an oligonucleotide derivative obtained by substituting cytosine with phenoxazine-modified cytosine in an oligonucleotide; an oligonucleotide derivative obtained by substituting ribose with 2'-O-propylribose in a DNA; and an oligonucleotide derivative obtained by substituting ribose with 2'-methoxyethoxyribose in the oligonucleotide.

29. (Previously Presented) A method for determining the expression level of a gene encoding a polypeptide according to any one of claims 1, 2, 3 and 51 by polymerase chain reaction, using an oligonucleotide selected from the following oligonucleotides: an oligonucleotide having an identical sequence to 10 to 50 contiguous nucleotides in a nucleotide sequence of DNA selected from a DNA encoding the

polypeptide according to any one of claims 1, 2, 3 and 51; a DNA having the nucleotide sequence represented by SEQ ID NO: 3; a DNA having the nucleotide sequence represented by SEQ ID NO: 4; and a DNA having the nucleotide sequence represented by SEQ ID NO: 5; and, an oligonucleotide having a complementary sequence to said oligonucleotide and a derivative of each of said oligonucleotides.

30. (Previously Presented) A method for detecting encephalopathy, renal diseases and cancers, using the method according to claim 26.

31. (Previously Presented) A method for suppressing the transcription of a DNA encoding a polypeptide according to any one of claims 1, 2, 3 and 51, using a DNA selected from a DNA encoding the polypeptide, a DNA having the nucleotide sequence represented by SEQ ID NO: 3, a DNA having the nucleotide sequence represented by SEQ ID NO: 4, and a DNA having the nucleotide sequence represented by SEQ ID NO: 5.

32. (Previously Presented) A method for suppressing the translation of an mRNA encoding a polypeptide according to any one of claims 1, 2, 3 and 51, using a DNA selected from a DNA encoding the polypeptide, a DNA having the nucleotide sequence represented by SEQ ID NO: 3, a DNA having the nucleotide sequence represented by SEQ ID NO: 4, and a DNA having the nucleotide sequence represented by SEQ ID NO: 5.

33. (Previously Presented) A method for suppressing the transcription of a DNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51, using an oligonucleotide selected from the following oligonucleotides: an oligonucleotide having an identical sequence to 10 to 50 contiguous nucleotides in a nucleotide sequence of DNA selected from a DNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51; a DNA having the nucleotide sequence represented by SEQ ID NO: 3; a DNA having the nucleotide sequence represented by SEQ ID NO: 4; and a DNA having the nucleotide sequence represented by SEQ ID NO: 5; and, an oligonucleotide having a complementary

sequence to said oligonucleotide and a derivative of each of said oligonucleotides.

34. (Previously Presented) A method for suppressing the translation of an mRNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51, using an oligonucleotide selected from the following oligonucleotides: an oligonucleotide having an identical sequence to 10 to 50 contiguous nucleotides in a nucleotide sequence of DNA selected from a DNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51; a DNA having the nucleotide sequence represented by SEQ ID NO: 3; a DNA having the nucleotide sequence represented by SEQ ID NO: 4; and a DNA having the nucleotide sequence represented by SEQ ID NO: 5; and, an oligonucleotide having a complementary sequence to said oligonucleotide and a derivative of each of said oligonucleotides.

35. (Previously Presented) An antibody recognizing a polypeptide according to any one of claims 1, 2, 3 and 51.

36. (Previously Presented) An immunoassay which detects a polypeptide according to any one of claims 1, 2, 3 and 51, using an antibody recognizing said polypeptide.

37. (Previously Presented) An immunohistological staining method which detects a polypeptide according to any one of claims 1, 2, 3 and 51, using an antibody recognizing said polypeptide.

38. (Previously Presented) A reagent for immunohistological staining which contains the antibody of claim 35.

39. (Previously Presented) An agent for diagnosing encephalopathy, renal diseases and cancers, which contains the antibody of claim 35.

40. (Previously Presented) A method for screening a substance that changes the activity of a polypeptide according to any one of claims 1, 2, 3 and 51, which comprises contacting said polypeptide with test samples.

41. (Previously Presented) A method for screening a substance that changes the expression of a gene encoding a polypeptide according to any one of claims 1, 2, 3 and 51, which comprises the steps of:

contacting a cell expressing said polypeptide with test samples, and

measuring the amount of the Lewis x or Lewis y sugar chain using an anti-Lewis x or anti-Lewis y antibody.

42. (Previously Presented) A method for screening a substance that changes the expression of a gene encoding a polypeptide according to any one of claims 1, 2, 3 and 51, which comprises the steps of:

contacting a cell expressing said polypeptide with test samples, and

measuring the amount of said polypeptide using an antibody recognizing said polypeptide.

43. (Previously Presented) A promoter DNA for the transcription of a gene encoding a polypeptide according to any one of claims 1, 2, 3 and 51.

44. (Previously Presented) The promoter DNA according to claim 43 which functions in a cell selected from the group consisting of neurons, kidney cells, gastric epithelium cells, leukocyte cells, cerebral tumor cells, neuroblastoma cells, melanoma cells, renal cancer cells, stomach cancer cells, colon cancer cells, and pancreatic cancer cells.

45. (Previously Presented) The promoter DNA according to claim 43 which is derived from human or mouse.

46. (Previously Presented) A method for screening a substance that changes the efficiency of transcription by a promoter DNA according to claim 43, which comprises the steps of:

transforming an animal cell with a plasmid comprising the promoter DNA and a reporter gene ligated downstream of said promoter DNA;

contacting transformant with a test sample; and

measuring the amount of the translation product of said reporter gene.

47. (Previously Presented) The screening method according to claim 46, wherein the reporter gene is a gene selected from the group consisting of chloramphenicol acetyltransferase genes, β-galactosidase genes, luciferase genes and green fluorescent protein genes.

48. (Previously Presented) A non-human knockout animal wherein a DNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51 is deleted or mutated.

49. (Previously Presented) The non-human knockout animal according to claim 48, wherein the non-human knockout animal is a mouse.

50. (Previously Presented) A method for treating renal diseases or cancers using a method according to claim 31.

51. (Previously Presented) The polypeptide according to claim 2, wherein the activity of transferring fucose to an N-acetylglucosamine residue in the Gal β 1-4GlcNAc structure existing in a nonreducing terminus of a sugar chain via an α 1,3-linkage is the Lewis x sugar chain [Gal β 1-4(Fuc α 1-3)GlcNAc] and the Lewis y sugar chain [Fuc α 1-2Gal β 1-4(Fuc α 1-3)GlcNAc] synthesizing activity, and the activity of transferring fucose to an N-acetylglucosamine residue in the NeuAc α 2-3Gal β 1-4GlcNAc structure

existing in a nonreducing terminus of a sugar chain via an α 1,3-linkage is the sialyl Lewis x sugar chain [NeuAc α 2-3Gal β 1-4(Fuc α 1-3)GlcNAc] synthesizing activity.

52. (Previously Presented) A non-human transformant or a transformant cell having the recombinant DNA according to claim 6.

53. (Previously Presented) The production method according to claim 18, wherein the complex carbohydrate is selected from the group consisting of glycoproteins, glycolipids, proteoglycans, glycopeptides, lipopolysaccharides, peptideglycans and glycosides wherein a sugar chain binds to steroids.

54. (Previously Presented) The production method according to claim 19, wherein the complex carbohydrate is selected from the group consisting of glycoproteins, glycolipids, proteoglycans, glycopeptides, lipopolysaccharides, peptideglycans and glycosides wherein a sugar chain binds to compounds such as steroids.

55. (Previously Presented) The production method according to claim 20, wherein the complex carbohydrate is selected from the group consisting of glycoproteins, glycolipids, proteoglycans, glycopeptides, lipopolysaccharides, peptideglycans and glycosides wherein a sugar chain binds to compounds such as steroids.

56. (Previously Presented) The production method according to claim 21, wherein the complex carbohydrate is selected from the group consisting of glycoproteins, glycolipids, proteoglycans, glycopeptides, lipopolysaccharides, peptideglycans and glycosides wherein a sugar chain binds to compounds such as steroids.

57. (Previously Presented) The production method according to claim 22, wherein the complex carbohydrate is selected from the group consisting of glycoproteins, glycolipids, proteoglycans, glycopeptides, lipopolysaccharides, peptideglycans and

glycosides wherein a sugar chain binds to compounds such as steroids.

58. (Previously Presented) The production method according to claim 23, wherein the complex carbohydrate is selected from the group consisting of glycoproteins, glycolipids, proteoglycans, glycopeptides, lipopolysaccharides, peptideglycans and glycosides wherein a sugar chain binds to compounds such as steroids.

59. (Previously Presented) A method for determining the expression level of a gene encoding a polypeptide according to any one of claims 1, 2, 3, and 51 by polymerase chain reaction, using an oligonucleotide selected from the following oligonucleotides: an oligonucleotide having an identical sequence to 10 to 50 contiguous nucleotides in a nucleotide sequence of DNA selected from a DNA encoding the polypeptide according to any one of claims 1, 2, 3, and 51; a DNA having the nucleotide sequence represented by SEQ ID NO: 3; a DNA having the nucleotide sequence represented by SEQ ID NO: 4; and a DNA having the nucleotide sequence represented by SEQ ID NO: 5; and, an oligonucleotide having a complementary sequence to said oligonucleotide and a derivative of each of said oligonucleotides,

wherein said oligonucleotide derivative is selected from the following oligonucleotide derivatives: an oligonucleotide derivative obtained by converting a phosphodiester bond into a phosphorothioate bond in an oligonucleotide; an oligonucleotide derivative obtained by converting a phosphodiester bond into a N3'-P5' phosphoamidate bond in an oligonucleotide; an oligonucleotide derivative obtained by converting a ribose and phosphodiester bond into a peptide-nucleic-acid bond in an oligonucleotide; an oligonucleotide derivative obtained by substituting uracil with C-5 propynyl uracil in an oligonucleotide; an oligonucleotide derivative obtained by substituting uracil with C-5 thiazolyl uracil in an oligonucleotide; an oligonucleotide derivative obtained by substituting cytosine with C-5 propynylcytosine in an oligonucleotide; an oligonucleotide derivative obtained by substituting cytosine with phenoxazine-modified cytosine in an oligonucleotide; an oligonucleotide derivative

obtained by substituting ribose with 2'-O-propylribose in a DNA; and an oligonucleotide derivative obtained by substituting ribose with 2'-methoxyethoxyribose in the oligonucleotide.

60. (Previously Presented) A method for suppressing the transcription of a DNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51, using an oligonucleotide selected from the following oligonucleotides: an oligonucleotide having an identical sequence to 10 to 50 contiguous nucleotides in a nucleotide sequence of DNA selected from a DNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51; a DNA having the nucleotide sequence represented by SEQ ID NO: 3; a DNA having the nucleotide sequence represented by SEQ ID NO: 4; and a DNA having the nucleotide sequence represented by SEQ ID NO: 5; and, an oligonucleotide having a complementary sequence to said oligonucleotide and a derivative of each of said oligonucleotides,

wherein said oligonucleotide derivative is selected from the following oligonucleotide derivatives: an oligonucleotide derivative obtained by converting a phosphodiester bond into a phosphorothioate bond in an oligonucleotide; an oligonucleotide derivative obtained by converting a phosphodiester bond into a N3'-P5' phosphoamidate bond in an oligonucleotide; an oligonucleotide derivative obtained by converting a ribose and phosphodiester bond into a peptide-nucleic-acid bond in an oligonucleotide; an oligonucleotide derivative obtained by substituting uracil with C-5 propynyl uracil in an oligonucleotide; an oligonucleotide derivative obtained by substituting uracil with C-5 thiazolyl uracil in an oligonucleotide; an oligonucleotide derivative obtained by substituting cytosine with C-5 propynylcytosine in an oligonucleotide; an oligonucleotide derivative obtained by substituting cytosine with phenoxazine-modified cytosine in an oligonucleotide; an oligonucleotide derivative obtained by substituting ribose with 2'-O-propylribose in a DNA; and an oligonucleotide derivative obtained by substituting ribose with 2'-methoxyethoxyribose in the oligonucleotide.

61. (Previously Presented) A method for suppressing the translation of an mRNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51, using an oligonucleotide selected from the following oligonucleotides: an oligonucleotide having an identical sequence to 10 to 50 contiguous nucleotides in a nucleotide sequence of DNA selected from a DNA encoding the polypeptide according to any one of claims 1, 2, 3 and 51; a DNA having the nucleotide sequence represented by SEQ ID NO: 3; a DNA having the nucleotide sequence represented by SEQ ID NO: 4; and a DNA having the nucleotide sequence represented by SEQ ID NO: 5; and, an oligonucleotide having a complementary sequence to said oligonucleotide and a derivative of each of said oligonucleotides,

wherein said oligonucleotide derivative is selected from the following oligonucleotide derivatives: an oligonucleotide derivative obtained by converting a phosphodiester bond into a phosphorothioate bond in an oligonucleotide; an oligonucleotide derivative obtained by converting a phosphodiester bond into a N3'-P5' phosphoamidate bond in an oligonucleotide; an oligonucleotide derivative obtained by converting a ribose and phosphodiester bond into a peptide-nucleic-acid bond in an oligonucleotide; an oligonucleotide derivative obtained by substituting uracil with C-5 propynyl uracil in an oligonucleotide; an oligonucleotide derivative obtained by substituting uracil with C-5 thiazolyl uracil in an oligonucleotide; an oligonucleotide derivative obtained by substituting cytosine with C-5 propynylcytosine in an oligonucleotide; an oligonucleotide derivative obtained by substituting cytosine with phenoxazine-modified cytosine in an oligonucleotide; an oligonucleotide derivative obtained by substituting ribose with 2'-O-propylribose in a DNA; and an oligonucleotide derivative obtained by substituting ribose with 2'-methoxyethoxyribose in the oligonucleotide.

62. (Previously Presented) The promoter DNA according to claim 44 which is derived from human or mouse.

63. (Previously Presented) A method for screening a substance that

changes the efficiency of transcription by a promoter DNA according to claim 44, which comprises the steps of:

transforming an animal cell with a plasmid comprising the promoter DNA and a reporter gene ligated downstream of said promoter DNA;

contacting transformant with a test sample; and

measuring the amount of the translation product of said reporter gene.

64. (Previously Presented) A method for screening a substance that changes the efficiency of transcription by a promoter DNA according to claim 45, which comprises the steps of:

transforming an animal cell with a plasmid comprising the promoter DNA and a reporter gene ligated downstream of said promoter DNA;

contacting transformant with a test sample; and

measuring the amount of the translation product of said reporter gene.

65. (Previously Presented) A method for screening a substance that changes the efficiency of transcription by a promoter DNA according to claim 62, which comprises the steps of:

transforming an animal cell with a plasmid comprising the promoter DNA and a reporter gene ligated downstream of said promoter DNA;

contacting transformant with a test sample; and

measuring the amount of the translation product of said reporter gene.

66. (Previously Presented) The screening method according to claim 63, wherein the reporter gene is a gene selected from the group consisting of chloramphenicol acetyltransferase genes, β-galactosidase genes, luciferase genes and green fluorescent protein genes.

67. (Previously Presented) The screening method according to claim 64,

wherein the reporter gene is a gene selected from the group consisting of chloramphenicol acetyltransferase genes, β-galactosidase genes, luciferase genes and green fluorescent protein genes.

68. (Previously Presented) The screening method according to claim 65, wherein the reporter gene is a gene selected from the group consisting of chloramphenicol acetyltransferase genes, β-galactosidase genes, luciferase genes and green fluorescent protein genes.

69. (Previously Presented) A method for treating renal diseases or cancers using a method according to claim 32.

70. (Previously Presented) A method for treating renal diseases or cancers using a method according to claim 33.

71. (Previously Presented) A method for treating renal diseases or cancers using a method according to claim 60.

72. (Previously Presented) A method for treating renal diseases or cancers using a method according to claim 34.

73. (Previously Presented) A method for treating renal diseases or cancers using a method according to claim 61.

74. (Previously Presented) A method for detecting encephalopathy, renal diseases and cancers, using the method according to claim 29.

75. (Previously Presented) A method for detecting encephalopathy, renal diseases and cancers, using the method according to claim 59.